

**REMARKS**

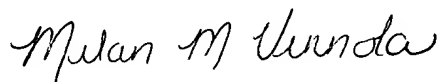
The claims have been amended to remove dependencies. However, such amendments are not intended to narrow the scope of the claims. No new matter enters by these amendments.

**CONCLUSION**

In view of the above, the presently pending claims are believed to be in immediate condition for allowance, and an indication of such is respectfully requested. The Examiner is invited to contact the undersigned at (202) 942-5000 with respect to any unresolved issues remaining in this application.

Applicants authorize a charge to Deposit Account Number 50-1824, referencing Attorney Docket No. 16515.102 for any fees (including fees for net addition of claims) related to the present application that are not otherwise provided for in the accompanying documents.

Respectfully submitted,



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### Marked-Up Claims

23. (Amended) A DNA construct comprising, as operably associated components in the 5' to 3' direction of transcription:

a promoter functional in a plant cell[,];

[a polynucleotide according to Claim 22,] a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2;

(b) a polynucleotide comprising SEQ ID NO: 1;

(c) a polynucleotide comprising a nucleotide sequence which has at least 70% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(d) a polynucleotide comprising a nucleotide sequence which has at least 80% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(e) a polynucleotide comprising a nucleotide sequence which has at least 90% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(f) a polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(g) a polynucleotide that hybridizes, under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and,

(h) a polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), (f), or (g); and,

a transcriptional termination sequence.

24. (Amended) A host cell comprising [the construct of Claim 23] a DNA construct comprising, as operably associated components in the 5' to 3' direction of transcription:

a promoter functional in a plant cell;

a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2;

(b) a polynucleotide comprising SEQ ID NO: 1;

(c) a polynucleotide comprising a nucleotide sequence which has at least 70% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(d) a polynucleotide comprising a nucleotide sequence which has at least 80% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(e) a polynucleotide comprising a nucleotide sequence which has at least 90% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(f) a polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(g) a polynucleotide that hybridizes, under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and,

(h) a polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), (f), or (g); and,

a transcriptional termination sequence.

26. (Amended) A plant comprising a cell [according to Claim 25] comprising a DNA construct comprising, as operably associated components in the 5' to 3' direction of transcription:

a promoter functional in a plant cell;

a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2;

(b) a polynucleotide comprising SEQ ID NO: 1;

- (c) a polynucleotide comprising a nucleotide sequence which has at least 70% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (d) a polynucleotide comprising a nucleotide sequence which has at least 80% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (e) a polynucleotide comprising a nucleotide sequence which has at least 90% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (f) a polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (g) a polynucleotide that hybridizes, under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and,
- (h) a polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), (f), or (g); and,
- a transcriptional termination sequence.

27. (Amended) A method for the alteration of the isoprenoid content in a plant, comprising:

[(a)] transforming said plant with a construct comprising as operably linked components[,];

a transcriptional initiation region functional in a plant[,];

[a polynucleotide according to Claim 22] a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2;
- (b) a polynucleotide comprising SEQ ID NO: 1;
- (c) a polynucleotide comprising a nucleotide sequence which has at least 70% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (d) a polynucleotide comprising a nucleotide sequence which has at least 80% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(e) a polynucleotide comprising a nucleotide sequence which has at least 90% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;  
(f) a polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;  
(g) a polynucleotide that hybridizes, under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and,  
(h) a polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), (f), or (g); and,  
a transcriptional termination region; and,  
[(b)] growing said plant, wherein said plant has said alteration of isoprenoid content.

32. (Amended) A method for producing an isoprenoid compound of interest in a plant cell, said method comprising:

[(a)] obtaining a transformed plant, said transformed plant having and expressing in its genome:

a primary construct comprising a DNA sequence encoding a polynucleotide comprising a transcriptional initiation region functional in a plant cell operably linked to [a polynucleotide according to Claim 22] a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2;
- (b) a polynucleotide comprising SEQ ID NO: 1;
- (c) a polynucleotide comprising a nucleotide sequence which has at least 70% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (d) a polynucleotide comprising a nucleotide sequence which has at least 80% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (e) a polynucleotide comprising a nucleotide sequence which has at least 90% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(f) a polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(g) a polynucleotide that hybridizes, under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and,

(h) a polynucleotide complementary to the polynucleotide sequence of (a),

(b), (c), (d), (e), (f), or (g); and,

at least one secondary construct comprising a DNA sequence encoding an isoprenoid enzyme operably linked to a transcriptional initiation region functional in a plant cell; and,

[(b)] growing said plant, wherein said plant produces said isoprenoid compound of interest.

34. (Amended) A method for increasing the non-mevalonate isoprenoid biosynthetic flux in a cell from a plant, said method comprising:

[(a)]transforming said plant with a construct comprising as operably linked components[.];

a transcriptional initiation region functional in a plant[.];

[a polynucleotide according to Claim 22,] a polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2;

(b) a polynucleotide comprising SEQ ID NO: 1;

(c) a polynucleotide comprising a nucleotide sequence which has at least 70% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(d) a polynucleotide comprising a nucleotide sequence which has at least 80% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(e) a polynucleotide comprising a nucleotide sequence which has at least 90% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(f) a polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;

(g) a polynucleotide that hybridizes, under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and,  
(h) a polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), (f), or (g); and,  
a transcriptional termination region; and,  
[(b)] growing said plant, wherein said plant has an increased non-mevalonate isoprenoid biosynthetic flux.

35. (Amended) A method for modulating disease resistance in a plant, comprising:

[(a)] introducing into said plant, a construct comprising [a polynucleotide according to Claim 22,] a polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO: 2;
- (b) a polynucleotide comprising SEQ ID NO: 1;
- (c) a polynucleotide comprising a nucleotide sequence which has at least 70% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (d) a polynucleotide comprising a nucleotide sequence which has at least 80% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (e) a polynucleotide comprising a nucleotide sequence which has at least 90% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (f) a polynucleotide comprising a nucleotide sequence which has at least 95% identity to that of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- (g) a polynucleotide that hybridizes, under stringent conditions to SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and,
- (h) a polynucleotide complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), (f), or (g); and,

[(b)] growing said plant, wherein said plant exhibits said modulated disease resistance.